Gene Ontology[™] (GO) Consortium

Jennifer I Clark

EMBL Outstation - European Bioinformatics Institute (EBI), Hinxton, Cambridge CB10 1SD, UK

Objectives: Build controlled vocabularies that allow researchers to describe gene products in a consistent way.

1) support the **annotation** of genomes, genes and gene products to these ontologies;

2) provide open and public access to the ontologies;

3) extend the **community** of people using GO.

Ontologies defined (for our purposes)

"an explicit specification of some topic" – Stanford Knowledge Systems Lab

Includes: vocabulary of terms (names for concepts in molecular biology) defined logical relationships between the terms.



Three ontologies in GO:

The GO Consortium produces three ontologies covering the concepts that could be described as:

• Molecular Function: elemental activity or task: DNA binding

• Biological Process: broad objective or goal: mitosis, signal transduction.

• Cellular Component: location or complex: nucleus, ribosome

Major factors in the success of the GO:

• **Open Source philosophy**, making all products available free of charge.

• The GO generates extraordinary cooperation between biologists from very **diverse fields of study**. Their commitment and focus has led to the development of a robust resource with the broadest application for the scientific community.





This annotation shows that HUCKLEBEIN protein is involved in the process of DNAdependent transcription. Term characteristics are inherited, so Transcription factor SL1 is understood also to be involved in DNA-dependent transcription and its parents.

Consortium members

Annotations are contributed by a growing number of biological database groups including:

The success of the GO Consortium's work has been to demonstrate the great utility of shared community ontologies in the genomics community. This success has inspired the development of similar ontologies for other domains and has promoted open collaborations among groups working on similar projects such as anatomies. These developments are now being collected under the general umbrella of OBO (**Open Biology Ontologies**, http://www.geneontology.org/doc/gobo.HTML).

WormBase FlyBase DictyBase Genome Knowledge Base Mouse Genome Database The Zebrafish Information Network Saccharomyces Genome Database TIGRGrameneRat Genome DatabaseCompugenGeneDB S. pombeGeneDB for protozoaEBI GOA projectThe Arabidopsis Information ResourceBerkeley Drosophila Genome ProjectThe Institute for Genomic Research



EBI Home Pagehttp://www.ebi.ac.ukGOhttp://www.geneontology.org/Email GO@geneontology.org



Telephone Fax +44(0) 1223 492600 +44(0) 1223 494468